

SEQUENCE LISTING

<110> Duke University
Lin, Haifan

<120> PURIFIED AND ISOLATED *piwi* FAMILY GENES AND GENE
PRODUCTS AND METHODS EMPLOYING SAME

<130> Attorney Docket No. 180-104 PCT

<140>

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<150> 60/110,091

<151> 1998-12-04

<160> 21

<170> PatentIn Ver. 2.1

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$\langle 222 \rangle \quad (84) \dots (2612)$

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Tyr	Thr	Arg	Arg	Asn	Tyr	Glu	Ala	Ala	Asn	Ser	Leu	Ile	Gln	Asn	Leu	
500			505						510			515				
ttt	aaa	gtt	aca	cca	gcc	atg	ggc	atg	caa	atg	aga	aaa	gca	ata	atg	1759
Phe	Lys	Val	Thr	Pro	Ala	Met	Gly	Met	Gln	Met	Arg	Lys	Ala	Ile	Met	
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Ile	Glu	Val	Asp	Asp	Arg	Thr	Glu	Ala	Tyr	Leu	Arg	Val	Leu	Gln	Gln	
			535						540			545				
aag	gtc	aca	gca	gac	acc	cag	ata	gtt	gtc	tgt	ctg	ttg	tca	agt	aat	1855
Lys	Val	Thr	Ala	Asp	Thr	Gln	Ile	Val	Val	Cys	Leu	Leu	Ser	Ser	Asn	
			550						555			560				
cgg	aag	gac	aaa	tac	gat	gct	att	aaa	aaa	tac	ctg	tgt	aca	gat	tgc	1903
Arg	Lys	Asp	Lys	Tyr	Asp	Ala	Ile	Lys	Lys	Tyr	Leu	Cys	Thr	Asp	Cys	
			565						570			575				
cct	acc	cca	agt	cag	tgt	gtg	gtg	gcc	cga	acc	tta	ggc	aaa	cag	caa	1951
Pro	Thr	Pro	Ser	Gln	Cys	Val	Val	Ala	Arg	Thr	Leu	Gly	Lys	Gln	Gln	
580			585						590			595				
act	gtc	atg	gcc	att	gct	aca	aag	att	gcc	cta	cag	atg	aac	tgc	aag	1999
Thr	Val	Met	Ala	Ile	Ala	Thr	Lys	Ile	Ala	Leu	Gln	Met	Asn	Cys	Lys	
			600						605			610				
atg	gga	gga	gag	ctc	tgg	agg	gtg	gac	atc	ccc	ctg	aag	ctc	gtg	atg	2047
Met	Gly	Gly	Glu	Leu	Trp	Arg	Val	Asp	Ile	Pro	Leu	Lys	Leu	Val	Met	
			615						620			625				
atc	gtt	ggc	atc	gat	tgt	tac	cat	gac	atg	aca	gct	ggg	cgg	agg	tca	2095
Ile	Val	Gly	Ile	Asp	Cys	Tyr	His	Asp	Met	Thr	Ala	Gly	Arg	Arg	Ser	
			630						635			640				
atc	gca	gga	ttt	gtt	gcc	agc	atc	aat	gaa	ggg	atg	acc	cgc	tgg	ttc	2143
Ile	Ala	Gly	Phe	Val	Ala	Ser	Ile	Asn	Glu	Gly	Met	Thr	Arg	Trp	Phe	
			645						650			655				
tca	cgc	tgc	ata	ttt	cag	gat	aga	gga	cag	gag	ctg	gta	gat	ggg	ctc	2191
Ser	Arg	Cys	Ile	Phe	Gln	Asp	Arg	Gly	Gln	Glu	Leu					

aaa gtc tgc ctg caa gcg gct ctg agg gct tgg aat agc tgc aat gag	2239
Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu	
680 685 690	
tac atg ccc agc cgg atc atc gtg tac cgc gat ggc gta gga gac ggc	2287
Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly	
695 700 705	
cag ctg aaa aca ctg gtg aac tac gaa gtg cca cag ttt ttg gat tgt	2335
Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys	
710 715 720	
cta aaa tcc att ggt aga ggt tac aac cct aga nta acg gta att gtg	2383
Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg Xaa Thr Val Ile Val	
725 730 735	
gtg aag aaa aga gtg aac acc aga ttt ttt gct cag tct gga gga aga	2431
Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg	
740 745 750 755	
ctt cag aat cca ctt cct gga aca gtt att gat gta gag gtt acc aga	2479
Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr Arg	
760 765 770	
cca gaa tgg tat gac ttt ttt atc gtg agc cag gct gtg aga agt ggt	2527
Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly	
775 780 785	
agt gtt tct ccc aca cat tac aat gtc atc tat gac aac agc ggc ctg	2575
Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu	
790 795 800	
aag cca gac cac ata cag cgc ttg acc tac aag ctg tgc cac atc tat	2623
Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr	
805 810 815	
tac aac tgg cca ggt gtc att cgt gtt cct gct cct tgc cag tac gcc	2671
Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala	
820 825 830 835	
cac aag ctg gct ttt ctt gtt ggc cag agt att cac aga gag cca aat	2719
His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn	
840 845 850	
ctg tca ctg tca aac cgc ctt tac tac ctc taacctgcag aagacgatgc	2769
Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu	
855 860	
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<210> 6

<211> 861

<212> PRT

<213> Homo sapiens

<400> 6

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Ile	Gln	Pro	Arg	Pro	Gln	Pro	Pro	Pro	Ala	Glu	Gly	Glu	Leu	Phe	Gly	35	40	45	
Arg	Gly	Arg	Gln	Arg	Gly	Thr	Ala	Gly	Gly	Thr	Ala	Lys	Ser	Gln	Gly	50	55	60	
Leu	Gln	Ile	Ser	Ala	Gly	Phe	Gln	Glu	Leu	Ser	Xaa	Ala	Glu	Arg	Gly	65	70	75	80
Gly	Arg	Arg	Arg	Asp	Phe	His	Asp	Leu	Gly	Val	Asn	Thr	Arg	Gln	Asn	85	90	95	
Leu	Asp	His	Val	Lys	Glu	Ser	Lys	Thr	Gly	Ser	Ser	Gly	Ile	Ile	Val	100	105	110	
Arg	Leu	Ser	Thr	Asn	His	Phe	Arg	Leu	Thr	Ser	Arg	Pro	Gln	Trp	Ala	115	120	125	
Leu	Tyr	Gln	Tyr	His	Ile	Asp	Tyr	Asn	Pro	Leu	Met	Glu	Ala	Arg	Arg	130	135	140	
Leu	Arg	Ser	Ala	Leu	Leu	Phe	Gln	His	Glu	Asp	Leu	Ile	Gly	Lys	Cys	145	150	155	160
His	Ala	Phe	Asp	Gly	Thr	Ile	Leu	Phe	Leu	Pro	Lys	Arg	Leu	Gln	Gln	165	170	175	
Lys	Val	Thr	Glu	Val	Phe	Ser	Lys	Thr	Arg	Asn	Gly	Glu	Asp	Val	Arg	180	185	190	
Ile	Thr	Ile	Thr	Leu	Thr	Asn	Glu	Leu	Pro	Pro	Thr	Ser	Pro	Thr	Cys	195	200	205	

Leu 210	Gln	Phe	Tyr	Asn	Ile	Ile 215	Phe	Arg	Arg	Leu 220	Lys	Ile	Met	Asn	
Leu 225	Gln	Gln	Ile	Gly	Arg	Asn 230	Tyr	Tyr	Asn	Pro 235	Asn	Asp	Pro	Ile	Asp 240
Ile	Pro	Ser	His	Arg 245	Leu	Val	Ile	Trp	Pro 250	Gly	Phe	Thr	Thr	Ser	Ile 255
Leu	Gln	Tyr	Glu 260	Asn	Ser	Ile	Met	Leu	Cys 265	Thr	Asp	Val	Ser	His	Lys
Val	Leu	Arg 275	Ser	Glu	Thr	Val	Leu 280	Asp	Phe	Met	Phe	Asn 285	Phe	Tyr	His
Gln 290	Thr	Glu	Glu	His	Lys	Phe 295	Gln	Glu	Gln	Val	Ser 300	Lys	Glu	Xaa	Ile
Gly 305	Leu	Val	Val	Leu	Thr 310	Lys	Tyr	Asn	Ile	Lys 315	Thr	Tyr	Arg	Val	Asp 320
Asp	Ile	Asp	Trp	Asp 325	Gln	Asn	Pro	Lys	Ser 330	Thr	Phe	Lys	Lys	Ala 335	Asp
Gly	Ser	Gly	Val 340	Ser	Phe	Leu	Glu	Tyr 345	Tyr	Arg	Lys	Gln	Tyr 350	Asn	Gln
Glu	Ile	Thr 355	Asp	Leu	Lys	Gln	Pro 360	Val	Leu	Val	Ser	Gln 365	Pro	Lys	Arg
Arg	Arg 370	Gly	Pro	Gly	Gly	Thr 375	Leu	Pro	Gly	Pro	Ala 380	Met	Leu	Ile	Pro
Glu 385	Leu	Cys	Tyr	Leu	Thr 390	Gly	Leu	Thr	Asp	Lys 395	Met	Arg	Asn	Asp	Phe 400
Asn	Val	Met	Lys	Asp 405	Leu	Ala	Val	His	Thr 410	Arg	Leu	Thr	Pro	Glu	Gln 415
Arg	Gln	Arg	Glu 420	Val	Gly	Arg	Leu	Ile 425	Asp	Tyr	Ile	His	Lys 430	Asn	Asp
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Gly 465	Gly	Lys	Thr	Phe	Asp 470	Tyr	Asn	Pro	Gln	Phe 475	Ala	Asp	Trp	Ser	Lys 480
Glu	Thr	Arg	Gly 485	Ala	Pro	Leu	Ile	Ser	Val 490	Lys	Pro	Leu	Asp	Asn	Trp 495
Leu	Leu	Ile	Tyr 500	Thr	Arg	Arg	Asn	Tyr 505	Glu	Ala	Ala	Asn	Ser	Leu	Ile
Gln	Asn	Leu 515	Phe	Lys	Val	Thr	Pro 520	Ala	Met	Gly	Met	Gln 525	Met	Arg	Lys

Ala	Ile	Met	Ile	Glu	Val	Asp	Asp	Arg	Thr	Glu	Ala	Tyr	Leu	Arg	Val	
530						535					540					
Leu	Gln	Gln	Lys	Val	Thr	Ala	Asp	Thr	Gln	Ile	Val	Val	Cys	Leu	Leu	
545					550					555					560	
Ser	Ser	Asn	Arg	Lys	Asp	Lys	Tyr	Asp	Ala	Ile	Lys	Lys	Tyr	Leu	Cys	
				565					570					575		
Thr	Asp	Cys	Pro	Thr	Pro	Ser	Gln	Cys	Val	Val	Ala	Arg	Thr	Leu	Gly	
			580					585					590			
Lys	Gln	Gln	Thr	Val	Met	Ala	Ile	Ala	Thr	Lys	Ile	Ala	Leu	Gln	Met	
		595					600					605				
Asn	Cys	Lys	Met	Gly	Gly	Glu	Leu	Trp	Arg	Val	Asp	Ile	Pro	Leu	Lys	
	610					615					620					
Leu	Val	Met	Ile	Val	Gly	Ile	Asp	Cys	Tyr	His	Asp	Met	Thr	Ala	Gly	
625					630					635					640	
Arg	Arg	Ser	Ile	Ala	Gly	Phe	Val	Ala	Ser	Ile	Asn	Glu	Gly	Met	Thr	
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			660					665					670			
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		675					680					685				
Cys	Asn	Glu	Tyr	Met	Pro	Ser	Arg	Ile	Ile	Val	Tyr	Arg	Asp	Gly	Val	
	690					695					700					
Gly	Asp	Gly	Gln	Leu	Lys	Thr	Leu	Val	Asn	Tyr	Glu	Val	Pro	Gln	Phe	
705					710					715					720	
Leu	Asp	Cys	Leu	Lys	Ser	Ile	Gly	Arg	Gly	Tyr	Asn	Pro	Arg	Xaa	Thr	
			725						730					735		
Val	Ile	Val	Val	Lys	Lys	Arg	Val	Asn	Thr	Arg	Phe	Phe	Ala	Gln	Ser	
			740					745					750			
Gly	Gly	Arg	Leu	Gln	Asn	Pro	Leu	Pro	Gly	Thr	Val	Ile	Asp	Val	Glu	
		755					760					765				
Val	Thr	Arg	Pro	Glu	Trp	Tyr	Asp	Phe	Phe	Ile	Val	Ser	Gln	Ala	Val	
	770					775					780					
Arg	Ser	Gly	Ser	Val	Ser	Pro	Thr	His	Tyr	Asn	Val	Ile	Tyr	Asp	Asn	
785					790					795					800	
Ser	Gly	Leu	Lys	Pro	Asp	His	Ile	Gln	Arg	Leu	Thr	Tyr	Lys	Leu	Cys	
				805					810					815		
His	Ile	Tyr	Tyr	Asn	Trp	Pro	Gly	Val	Ile	Arg	Val	Pro	Ala	Pro	Cys	
			820					825					830			
Gln	Tyr	Ala	His	Lys	Leu	Ala	Phe	Leu	Val	Gly	Gln	Ser	Ile	His	Arg	
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Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
850 855 860

<210> 7

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 7

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42

<210> 8

<211> 42

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42

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<211> 45

<212> DNA

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<223> Description of Artificial Sequence: Synthesized
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45

<210> 10

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
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45

<210> 11

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<212> DNA

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<223> Description of Artificial Sequence: Synthesized
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17

<210> 12

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 12

tgcaactgcca ggtccttcat cac

23

<210> 13

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 13

ggccagtcac tttccagtca gctcaggtg

29

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 14

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20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 15

tgcccatata catcaccatc

20

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthesized
Oligonucleotide Primer

<400> 16

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24

<210> 17
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23

<210> 18
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24

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24

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20250404 14:00:00

<400> 20

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20

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<223> Description of Artificial Sequence: linker peptide

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PPRQ

4